09/192, 292

WEST Search History

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DATE: Saturday, June 08, 2002

Set Name side by side	Query	Hit Count	Set Name result set
	DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=OR		
L6	L1 same support	47	L6
L5	L4 not L3	18	L5
L4	L1 same tag	18	L4
L3	L1 same capture	7	L3
L2	L1 same array	12	L2
L1	universal with (oligonucleotide or polynucleotide)	650	L1

END OF SEARCH HISTORY

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L2: Entry 3 of 12   File: PGPB   Jan 31, 2002

DOCUMENT-IDENTIFIER: US 20020012926 A1
TITLE: Combinatorial array for nucleic acid analysis

Summary of Invention Paragraph (2):
[0003] This invention relates in general to an array, including a universal array, for
the analysis of nucleic acids, such as DNA. The devices and methods of the invention
can be used for identifying gene expression patterns in any organism. More
specifically, the universal arrays of the invention comprise oligonucleotide probes of
all possible oligonucleotide sequences having a specified length n that may be selected
by a user. The invention also relates to analytical methods which can be used to
analyze data (e.g., hybridization data) from such arrays.

Summary of Invention Paragraph (17):
[0018] A further object of the invention is to provide a universal micro-array; i.e.,
an array of oligonucleotides having a specified sequence length n (referred to herein
as "n-mers") wherein all possible nucleotide sequence of length n are present on the
array. Current technologies use chips having only certain specific oligonucleotides
that are carefully selected to detect particular genes. Thus, for every organism (or
even for different cells from the same organism that express different genes) it is
necessary to design a new micro-array. The universal arrays of this invention therefore
offer the advantage of being useful for studying gene expression in any cell or
organism; thereby making a specially designed chip unnecessary.

Summary of Invention Paragraph (18):
[0019] Still another object of the invention is to determine and provide useful values
for the oligonucleotide sequence length n that may be used in a universal array,
particularly for preferred embodiments of analyzing gene expression.

Summary of Invention Paragraph (23):
[0024] The invention is based in part on the inventors' discovery that appropriate
probe lengths n may be selected that are small enough that fabrication of universal
micr-arrays comprising all oligonucleotide probe sequence of length n is feasible and
average probe "degeneracy" is low (i.e., each probe only hybridizes to, on average,
only a few nucleic acids or genes). As a result, a hybridization matrix describing the
"mapping" of expression levels to hybridization data in an experiment may be easily
deconvoluted using the algorithms of the invention to identify relatively small
subblocks.

Detail Description Paragraph (50):
[0084] The universal array of the present invention consists of a regular pattern of
distinct spots of DNA sequences, each spot containing oligonucleotide strands of length
n. In the set

Detail Description Paragraph (132):
[0162] It is noted that the methods of the invention are not limited to the particular
mismatch model described above and that other models, which will be readily apparent to
the skilled artisan, may also be used. For exdample, a variety of thermodynamic models
for nucleic hybridization are well known in the art [1, 6, 8, 14, 18]. Using such
models, a skilled artisan may readily determine (e.g, by calculation) a number of
sequences c(n) of length n that will hybridize or are capable of hybridizing to an
oligonucleotide probe of length n. Thus, for a given collection of No different
oligonucleotide probes having a particular sequence length n (for example, a collection
of $N.sub.0=4.sup.n$ probes on a universal array) the number of sequences <c(n)> that may
hybridize, on average, to a given probe can be readily calculated or otherwise
determined. The probability of binding is expected to increase by this factor so that

the average probe degeneracy may be provided by the relation 9 d (n) = N g N 0 (1 - n + L) .times. c (n)

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L5: Entry 5 of 18   File: USPT   Jul 18, 2000

DOCUMENT-IDENTIFIER: US 6090549 A
TITLE: Use of continuous/contiguous stacking hybridization as a diagnostic tool

Detailed Description Paragraph Right (15):
In addition to the use of universal base or four-base approach, different mobile oligonucleotides, among the 1024 possibilities in the case of a pentamer mobile fraction, can be labeled with different fluorochromes. In the case of two different labels, the number of hybridizations will decrease by a factor of two. In the case of four different labels, the number of required hybridizations will decrease by a factor of four. This use of different labels is illustrated in FIGS. 2 and 3 whereby the geometric shapes of a circle, triangle, pentagon and square graphically represent different tags or fluorochromes.